isoelectric focusing analysis, polymerase chain reaction and sequencing, we detected the major genotypic characterization of ESBLs was CTX-M-14 (76.2%). Two strains showed indistinguishable patterns by pulsed-field gel electrophoresis.

Conclusion: This study documented the CTX-M family as the predominant ESBL type among Macao population. The spread of CTX-M enzymes is concerning and deserves close monitoring in further investigation.

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23.017

Utilizing hospital generated antibiograms to examine state trends in antibiotic resistance

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Background: Antibiograms are aggregated, hospital-generated reports on susceptibility of bacteria of interest to specific antibiotics. They are utilized within hospitals to assist in effective use of antibiotics. The Massachusetts Department of Public Health (MDPH) has been requesting voluntary submission of antibiograms from hospitals annually since 1999.

Methods: Susceptible proportions reported in antibiograms were analyzed to evaluate changes in levels of susceptibility over five years, while accounting for the effect of hospital characteristics. Trends were examined for specific antibiotic and bacteria combinations as well as antibiotic class susceptibility patterns. Data were analyzed using SAS software version 9.1 (SAS Institute Inc., USA).

Results: Significant trends in antibiotic resistance were seen with a strong decreasing trend in *E.coli* fluoroquinolone-susceptibility and a moderate decrease in *Klebsiella pneumoniae* and *Enterobacter cloacae*. Specifically, *E.coli* susceptibility to ciprofloxacin decreased substantially over five years, and this trend was more pronounced in specific regions of the state. Other hospital characteristics such as bed count and hospital type did not appear to have a significant association with antibiotic resistance trends.

Conclusion: Antibiograms may serve as useful tools in examining regional antibiotic resistance trends. Trends identified may be used to inform further studies and pinpoint areas of concern for hospitals.

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23.018

A Comparative study on gram-negative bacterial infections in Mansoura University Hospitals, Egypt

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Background: Gram negative bacteria are responsible for numerous infectious diseases. These diseases can occur in and harm any part of the body, the skin, eyes and the nervous, cardiovascular, respiratory, gastrointestinal and urogenital systems.

Methods: In the present study, some phenotyic and molecular typing techniques were applied on 108 strains of *E. coli*, 88 strains of *Ps. aeruginosa* and 8 strains of *Serratia* isolated from different clinical lesions in Mansoura University Hospitals, Egypt.

Results: The distribution of antibiotic resistance among the isolated strains showed high incidence of resistance and imipenem was the most active antibiotic. Using the active pyocin typing, 72 strains of *Ps. aeruginosa* could be typed into 35 pyotypes. SDS-PAGE of total cell protein extracts showed that the presence of fifteen patterns among *E. coli* strains and eleven patterns among *Ps. aeruginosa* strains. Using PCR technique it was found that 84% of the 50 tested strains were found to have at least one of the tested ESBLs. Also *TolC* and *AcrA* genes were present in all tested *E. coli* except 4 strains and did not present in *Ps. aeruginosa* except 4 strains. Plasmid profiles of 23 tested *E. coli* appear to be diverse. Also the prevalence of plasmids in 22 tested *Ps. aeruginosa* strains was lower than in tested *E. coli* therefore 59.1% of tested Ps. aeruginosa strains harbored plasmids. Using Pyrosequencing technique, the sequenced region of *gyrA*, *gyrB* and *ParC* were able to differentiate between the tested strains and neighbor-joining tree was constracted to determine relatedness between the isolated strains. Morover, Molecular cloning of the whole sequence of *bla-TEM*, *bla-SHV* and *bla-CTX-M* was carried out experimentally to study the expression of these genes and determine which genes of them responsible for the resistance.

Conclusion: Molecular-based methods of typing are more advantageous compared with phenotypic methods of typing in terms of better discrimination and reproducibility. Significant genetic variation was observed among different strains represented by the diversity of their plasmid profiles. All molecular genetic methods for distinguishing organism subtypes are based on differences in the DNA sequence.

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23.019

Extended spectrum beta-lactamases in *Escherichia coli* and *Klebsiella* spp. from Eastern Romania

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Background: The emergence and dissemination of ESBL are problems of major importance for the population health; ESBLs represent a first example of factor that contribute to the global crisis concerning the treatment of *Klebsiella pneumoniae* and *Escherichia coli* against which the third generation cephalosporins are not efective anymore.

Methods: Clinically isolates of E. coli (n= 642) and *Klebsiella* (n=92) were collected from patients with different types of infections (sepsis, urinary tract infections,